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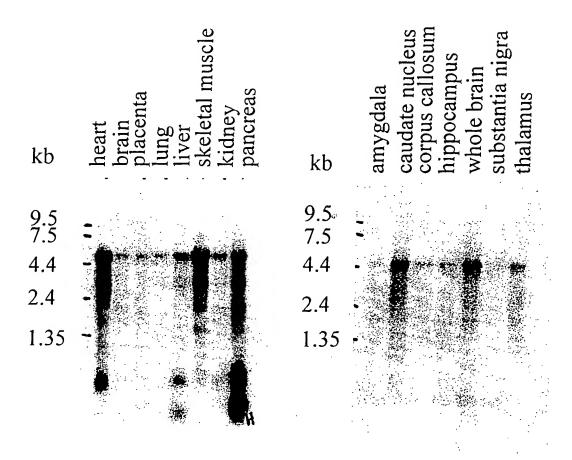
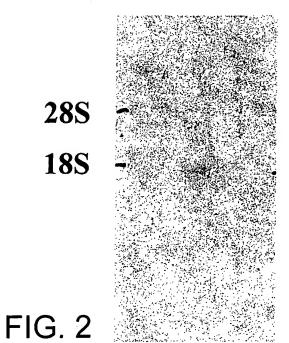


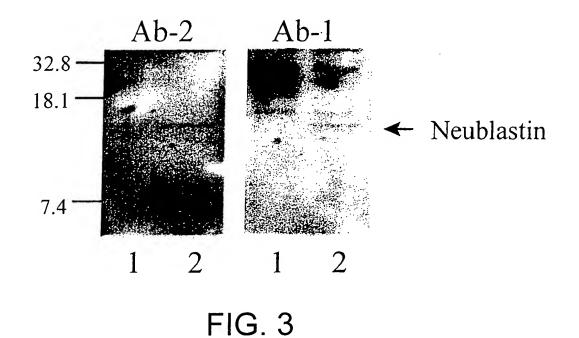
FIG. 1A

FIG. 1B

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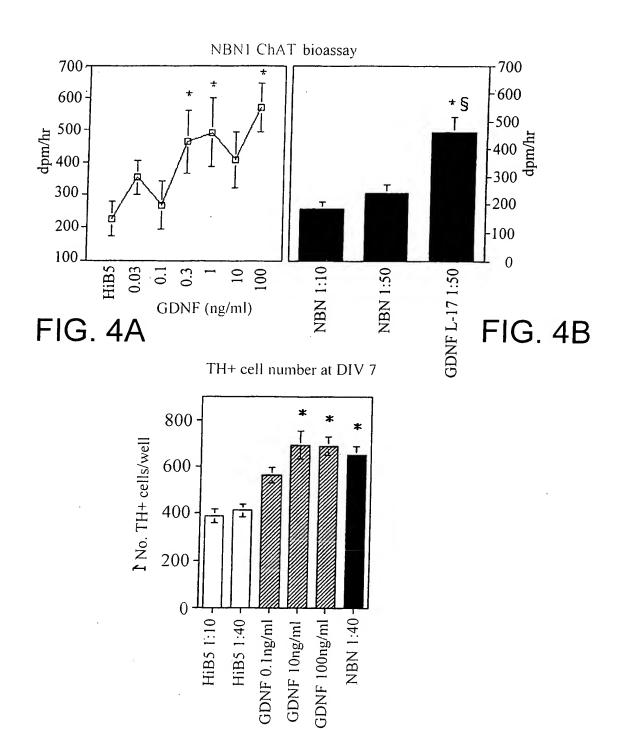
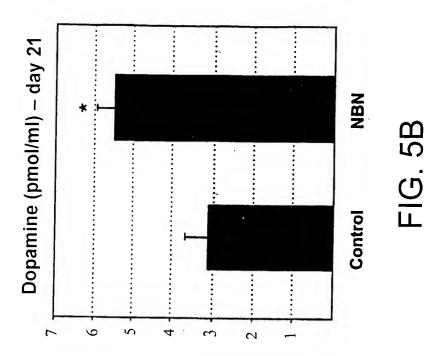
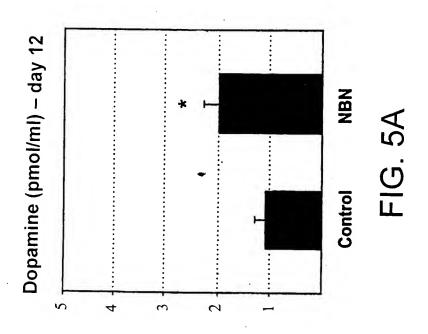


FIG. 4C

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TH-ir cells per culture

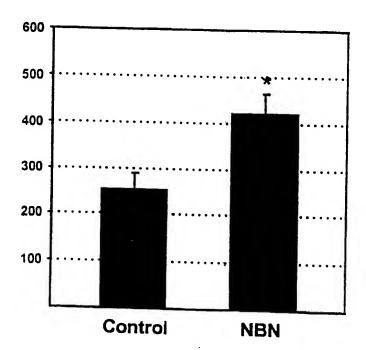


FIG. 5C

%FG lesion/intact

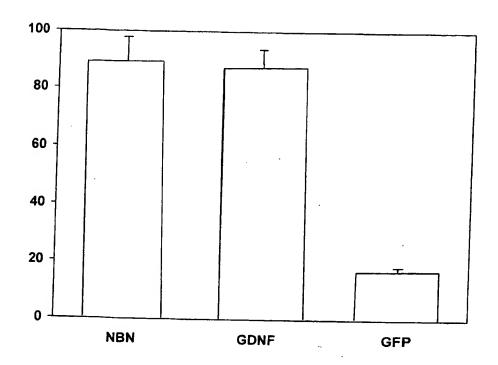
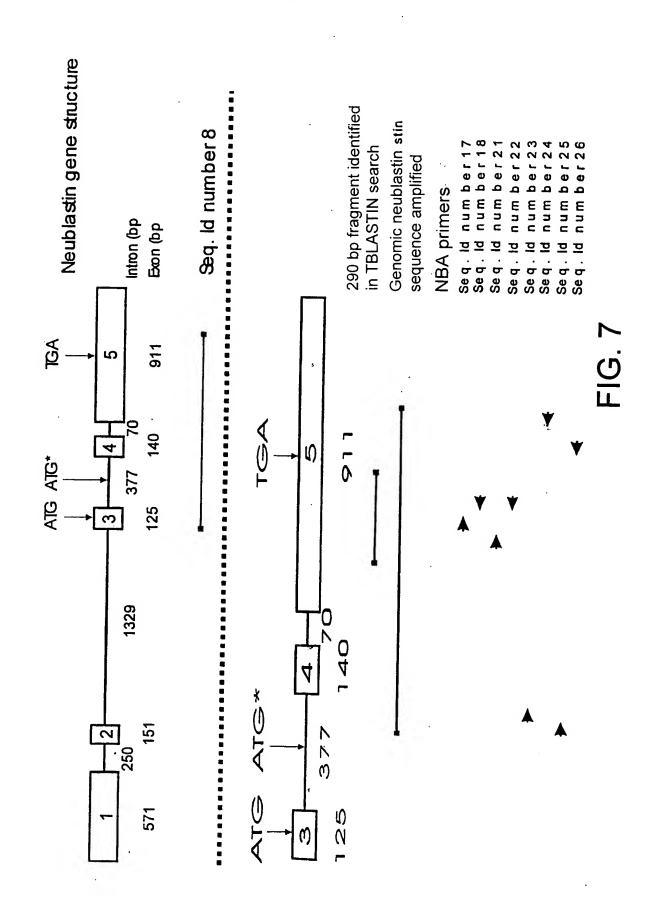


FIG. 6

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Alignment of Neublastin primers used in Rapid-Screen with homologous regions in other GDNF ligands

5'-C	CTG	GCC	AGC	CTA	CTG	GG-3′	SEQ ID No 17
G	CTG	GCC	C G G	CTG	CAG	GG	persephin
G	CTG	CGA	CGA	CTG	CGC	CA	neurturin
A	TTG	AAA	AAC	TTA	TCC	AG	GDNF

5′-	AA	GGA	GAC	CGC		TTC	GTA	GCG-3'	SEQ ID No 18
	TA	GGC	CAC	GTC		GGT	GTA	GCG	persephin
	AA	GGA	CAC	CTC	GTC	CTC	GTA	G GC	neurturin
	AA	CGA	CAG	GTC	ATC	ATC	AAA	GGC	GDNF

conserved nucleotides shown in bold

FIG. 8

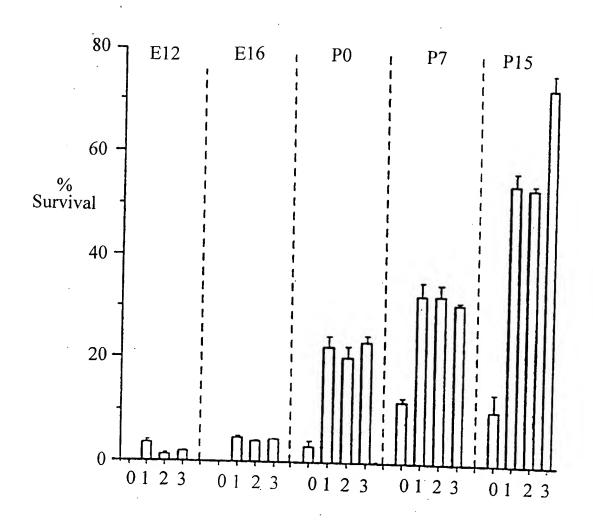
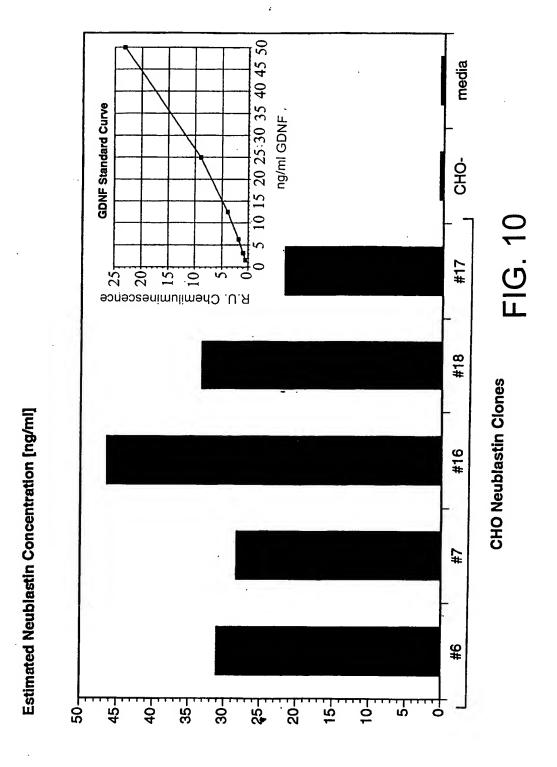


FIG. 9

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Relative Chemiluminesence Units (R.U.)

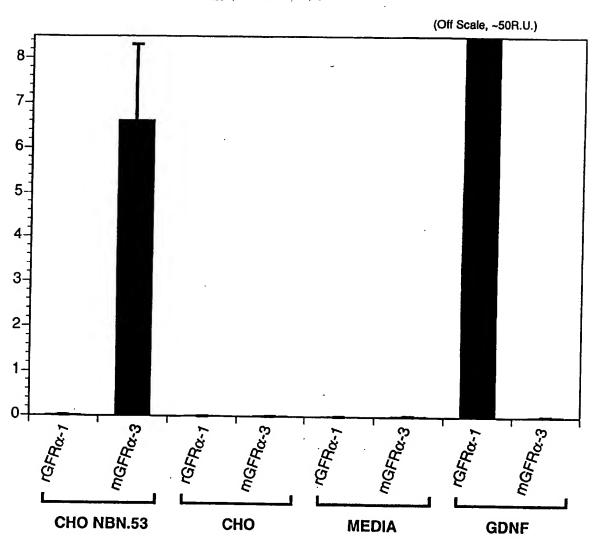
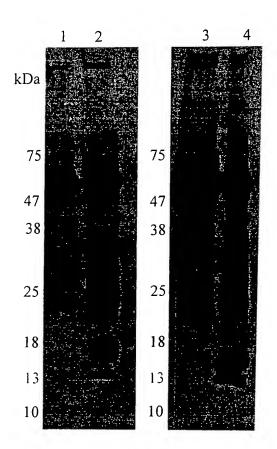


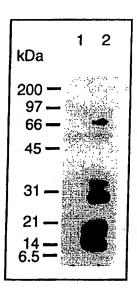
FIG. 11



- 1. Control medium stained with R30 anti-peptide antibody
- 2. Neublastin containing conditioned medium stained with R30 anti-peptide antibody
- 3. Control medium stained with R31 anti-peptide antibody
- 4. Neublastin containing conditioned medium stained with R31 anti-peptide antibody

FIG. 12

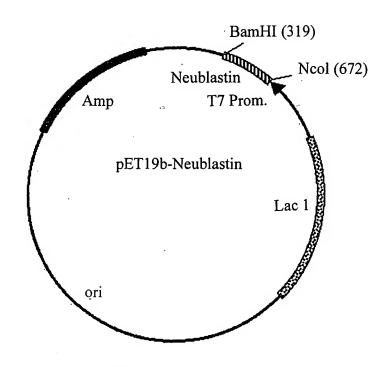
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Extraction of neublastin by affinity-binding on RETL3-Ig Lane 1: bound from CHO control conditioned media Lane 2: bound from neublastin overexpressing CHO conditioned media

FIG. 13

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Neublastin Syngene

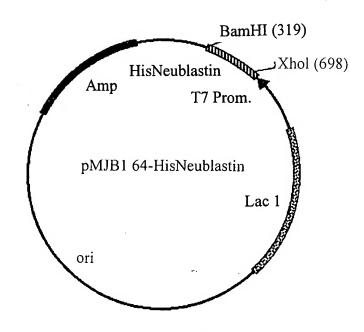
	N	lcoi	(318)																	
316	TAC	CAT	GGCT	GGA	GGA	CCGG	G2	ATCI	rcgi	'GC	TCGI	GC.	AGCA	GGZ	GCA	ССТС	GC	ייתים	reco	ייים
											AGCA									
		M		G	G	Р			R			Α.			A	R	G		R	ıGA
	•		••	~	~	•	_	·	• • •	^		\sim	^	u	^	n	G	C	n	L
376	GCG	TTC	FCAA	CTA	GTG	CCGG	TO	CGI	GCA	CT	CGGA	CTC	GGA	CAC	CGT	TCCG	AC	GAA	CTA	GT
	CGC	AAG	AGTT	GAT	CAC	GGCC	AC				GCCTGACCCT			GTG	TGCTTGATCA					
19			Q	L	٧	Р	V				G					S		E	L	٧
136	3.00	mmma																		
450	TOO		CGT	TTT	TGT	TCAG	GA	TCT	TGT	CG	TCGT	GCA	CGT	TCT	CCG	CATG	AT	CTA	TCT	'CT
افد	TGC.	AAAA	AGCA	AAA F	ACA								AGAGGCGTAC			TAGATAGAGA			.GA	
39	n	F	R	۲	С	S	G	S	С	R	R	Α	R	S	Р	Н	Ð	L	S	L
496	AGC	ATCI	CTA	CTA	GGA	GCCG	GA	GCA	СТА	AG	ACCG	ccc	CCG	GGA	ጥርጥ	A C A C	CT	~m×	m c m	C 3
	TCG	rag <i>a</i>	GAT	GAT	CCT	CGGC	СТ	CGT	CAT	TC	TGGC	GGC	GGC	CCM	BCB:	MCMC	CI	GIM	101	CA
59	Α .	S	L	L				A		R	P				S	R		V	AGA S	
			_	_	_	••	_	••	_	• • •	•	•	•	u	3	п	F	٧	3	Q
											• •									
556							GA	TAC	GAA	GC	AGTA	TCT	TTC	ATG	GAC	GTAA	AC'	гст	ACA	TG
	_	_				TGAT					TCAT.	AGA.	AAG	TAC	CTG	CATT	TG	AGA	TGT	AC
79 🕨	Р	С	С	R	P	T	R	Υ	Ε	Α	V	S	F	М	D	V	N	S	T	W
																			D	ш и

BamHI (671)

616 GAGAACCGTA GATAGACTAT CTGCAACCGC ATGTGGCTGT CTAGGATGAT AATAGGGATC CTCTTGGCAT CTATCTGATA GACGTTGGCG TACACCGACA GATCCTACTA TTATCCCTAG

676 CGGCT GCCGA

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HisNeublastin

Xhol (340)

							Xnoi (340)														
301	TACC	ATG	GGC	CAT	CAT	CATC	AT	CAT	CAT	CA	TCAT	CAT	CAC	TCG	ATATCGACGA						
	ATCC	TAC	CCG	GTA	GTA	GTAG	TAGTAGTAGT			GT	AGTAGTAGTG			AGC	CCGG	TATAGCTGCT					
	1 🕨		G	Н	Н	Н		Н		Н			H		S		Н	1	D	D	
	1,	141	u	• • •	••	• •	••	••	••	• •	* *	• •									
361	CGAC	GAC	AAG	GCT	GGA	GGAC	CG	GGA	TCT	CG	TGCT	CGT	GCA	GCA	GGA	GCAC	GT	GGC	TGT	CG	
• • -	GCTG	CTG	TTC	CGA	CCT	CCTG	GC	CCT	AGA	GC	ACGA	GCA	CGT	CGT	CCT	CGTG	CA	CCG	ACAGC		
19		ח	K	A	_	G	Р		S			R		Α.			R	G		R	
17,			• • • • • • • • • • • • • • • • • • • •	•	•	_		_		• •											
421	TCTGCGTTCT CAACTAGTGC					CGGTGCGTGC				ACTCGGACTG			GGA	CCGACGAACT							
	AGAC	GCA.	AGA	GTT	GAT	CACG	GC	CAC	GCA	.CG	TGAG	CCT	GAC	CCT	GTG	GCAA	GG	CTG	CTT	GA	
39		R		Q		V	Ρ	٧		Α	L	G	L	G		R	S		Ε		
33.	_	• •	_	_	-	-															
481											TCGT										
	TCAT	GCA.	AAA	GCA	AAA	ACAA	GT	CCT	AGA	AC	AGCA	GCA	CGT				TA	CTA	GAT	AG	
59	V	R	F	R	F	С	S	G	S	C	R	R	Α	R	S	Р	Н	D	L	S	
																	~-				
541							CCGGAGCACT														
	AGAT	CGT	AGA	GAT	GAT	CCTC	GG	CCT	CGT	GA	TTCT										
79	L	Α	S	L	L	G	Α	G	Α	L	R	Р	P	Р	G	S	R	Р	٧	S	

601 TCAACCTTGT TGTAGACCTA CTAGATACGA AGCAGTATCT TTCATGGACG TAAACTCTAC
AGTTGGAACA ACATCTGGAT GATCTATGCT TCGTCATAGA AAGTACCTGC ATTTGAGATG

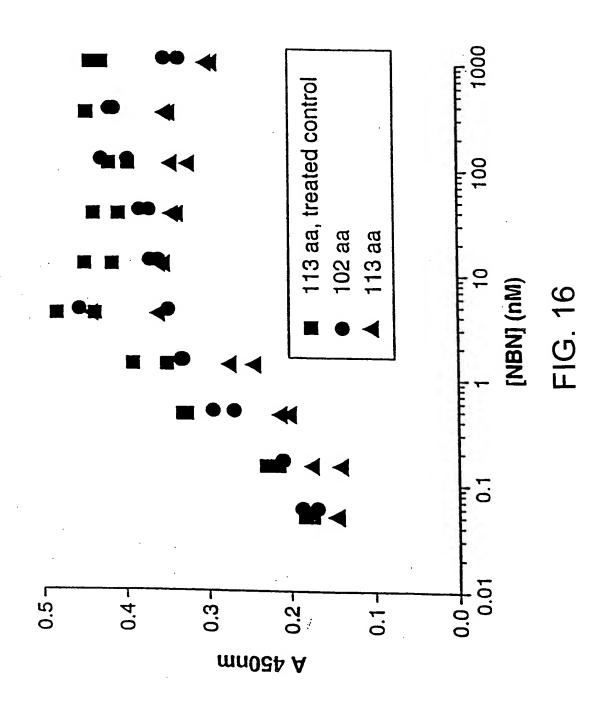
99 ▶ Q P C C R P T R Y E A V S F M D V N S T

BamHI (719)

- ATGGAGAACC GTAGATAGAC TATCTGCAAC CGCATGTGGC TGTCTAGGAT GATAATAGGG
 TACCTCTTGG CATCTATCTG ATAGACGTTG GCGTACACCG ACAGATCCTA CTATTATCCC

 119 W R T V D R L S A T A C G C L G •
- 721 ATCCGGCTGC TAACAAAGCC CG
 TAGGCCGACG ATTGTTTCGG GC

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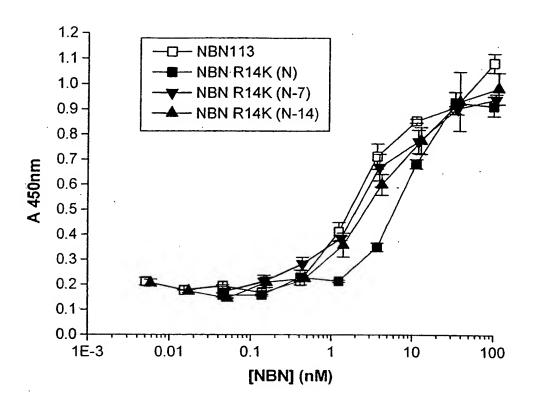


FIG. 17

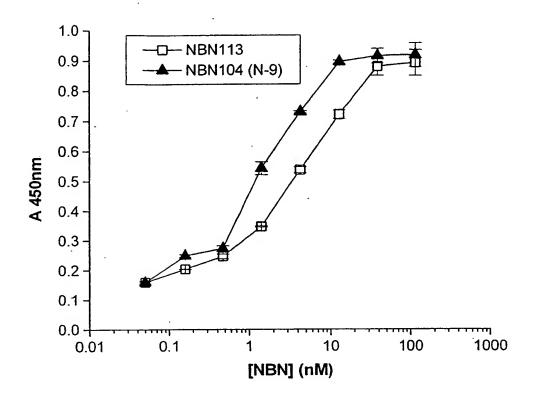


FIG. 18